



## SEQUENCE LISTING

<110> ADLER, JON ELLIOT  
LI, XIAODONG  
STASZEWSKI, LENA  
O'CONNELL, SHAWN  
ZOZULYA, SERGEY

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<141> 2002-01-03

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<170> PatentIn Ver. 3.3

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Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val  
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<213> Rattus sp.

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&lt;210&gt; 16

&lt;211&gt; 2526

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 16

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<210> 17
<211> 841
<212> PRT
<213> Homo sapiens

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<400> 17
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Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
 20              25              30

Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
 35              40              45

Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
 50              55              60

Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
 65              70              75              80

Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
 85              90              95

Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
100              105              110

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Tyr	Ala	Thr	Leu	Arg	Val	Leu	Ser	Leu	Pro	Gly	Gln	His	His	Ile	Glu	115	120	125
Leu	Gln	Gly	Asp	Leu	Leu	His	Tyr	Ser	Pro	Thr	Val	Leu	Ala	Val	Ile	130	135	140
Gly	Pro	Asp	Ser	Thr	Asn	Arg	Ala	Ala	Thr	Thr	Ala	Ala	Leu	Leu	Ser	145	150	155
Pro	Phe	Leu	Val	Pro	Met	Ile	Ser	Tyr	Ala	Ala	Ser	Ser	Glu	Thr	Leu	165	170	175
Ser	Val	Lys	Arg	Gln	Tyr	Pro	Ser	Phe	Leu	Arg	Thr	Ile	Pro	Asn	Asp	180	185	190
Lys	Tyr	Gln	Val	Glu	Thr	Met	Val	Leu	Leu	Leu	Gln	Lys	Phe	Gly	Trp	195	200	205
Thr	Trp	Ile	Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly	210	215	220
Val	Gln	Ala	Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala	225	230	235
Phe	Lys	Asp	Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met	245	250	255
Gln	Cys	Leu	Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val	260	265	270
Val	Phe	Ser	Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val	275	280	285
Leu	Thr	Asn	Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Ala	290	295	300
Leu	Ser	Arg	His	Ile	Thr	Gly	Val	Pro	Gly	Ile	Gln	Arg	Ile	Gly	Met	305	310	315
Val	Leu	Gly	Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala	325	330	335
Phe	Glu	Glu	Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Lys	Ala	Pro	Arg	Pro	Cys	340	345	350
His	Lys	Gly	Ser	Trp	Cys	Ser	Ser	Asn	Gln	Leu	Cys	Arg	Glu	Cys	Gln	355	360	365
Ala	Phe	Met	Ala	His	Thr	Met	Pro	Lys	Leu	Lys	Ala	Phe	Ser	Met	Ser	370	375	380
Ser	Ala	Tyr	Asn	Ala	Tyr	Arg	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu	385	390	395
His	Gln	Leu	Leu	Gly	Cys	Ala	Ser	Gly	Ala	Cys	Ser	Arg	Gly	Arg	Val	405	410	415

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu  
 420 425 430  
 His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser  
 435 440 445  
 Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr  
 450 455 460  
 Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu  
 465 470 475 480  
 Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val  
 485 490 495  
 Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe  
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 His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu  
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 Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu  
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 Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu  
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 Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly  
 610 615 620  
 Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu  
 625 630 635 640  
 Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu  
 645 650 655  
 Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala  
 660 665 670  
 Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala  
 675 680 685  
 Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu  
 690 695 700  
 Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys  
 705 710 715 720

Thr	Glu	Thr	Asn	Ser	Leu	Gly	Phe	Ile	Leu	Ala	Phe	Leu	Tyr	Asn	Gly	725	730	735
Leu	Leu	Ser	Ile	Ser	Ala	Phe	Ala	Cys	Ser	Tyr	Leu	Gly	Lys	Asp	Leu	740	745	750
Pro	Glu	Asn	Tyr	Asn	Glu	Ala	Lys	Cys	Val	Thr	Phe	Ser	Leu	Leu	Phe	755	760	765
Asn	Phe	Val	Ser	Trp	Ile	Ala	Phe	Phe	Thr	Thr	Ala	Ser	Val	Tyr	Asp	770	775	780
Gly	Lys	Tyr	Leu	Pro	Ala	Ala	Asn	Met	Met	Ala	Gly	Leu	Ser	Ser	Leu	785	790	795
Ser	Ser	Gly	Phe	Gly	Gly	Tyr	Phe	Leu	Pro	Lys	Cys	Tyr	Val	Ile	Leu	805	810	815
Cys	Arg	Pro	Asp	Leu	Asn	Ser	Thr	Glu	His	Phe	Gln	Ala	Ser	Ile	Gln	820	825	830
Asp	Tyr	Thr	Arg	Arg	Cys	Gly	Ser	Thr								835	840	

<210> 18

<211> 14

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$

<223> Description of Artificial Sequence: Consensus sequence

$\langle 220 \rangle$

<221> MOD RES

$\langle 222 \rangle$  (1)

<223> Thr or Arg

<220>

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<221> MOD RES
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<222> (3)

<223> Phe or Leu

$\langle 220 \rangle$

&lt;221&gt; MOD\_RES

<222> (4)

<223> Arg, Gln or Pro

<220>

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<221> MOD_RES
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<222> (6)

<223> Arg or Thr

<220>

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<221> MOD_RES
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<222> (7)

<223> Ser, Pro or Val

<220>  
 <221> MOD\_RES  
 <222> (8)  
 <223> Val, Glu, Arg, Lys or Thr

<220>  
 <221> MOD\_RES  
 <222> (11)  
 <223> Ala or Glu

<220>  
 <221> MOD\_RES  
 <222> (12)  
 <223> Trp or Leu

<220>  
 <221> MOD\_RES  
 <222> (13)  
 <223> Arg, His or Gly

<400> 18  
 Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu  
           1                  5                  10

<210> 19  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Consensus  
           sequence

<220>  
 <221> MOD\_RES  
 <222> (1)  
 <223> Leu or Gln

<220>  
 <221> MOD\_RES  
 <222> (3)  
 <223> Glu, Gly or Thr

<220>  
 <221> MOD\_RES  
 <222> (4)  
 <223> Asn, Arg or Cys

<220>  
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<220>  
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<220>  
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 <223> Cys, Gly or Phe

<220>  
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 <222> (11)  
 <223> Val, Leu or Ile

<220>  
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 <222> (13)  
 <223> Phe or Leu

<220>  
 <221> MOD\_RES  
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 <223> Ala or Ser

<220>  
 <221> MOD\_RES  
 <222> (15)  
 <223> Met or Leu

<400> 19  
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<210> 20  
 <211> 2520  
 <212> DNA  
 <213> Homo sapiens

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<210> 21  
 <211> 839  
 <212> PRT  
 <213> Homo sapiens

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 Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile  
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 Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val  
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 Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu  
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 Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr  
                     85                    90                    95  
 Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu  
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 Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr  
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Gln	Ile	Thr	Tyr	Ser	Ala	Ile	Ser	Asp	Glu	Leu	Arg	Asp	Lys	Val	Arg	165	170	175	
Phe	Pro	Ala	Leu	Leu	Arg	Thr	Thr	Pro	Ser	Ala	Asp	His	His	Val	Glu	180	185	190	
Ala	Met	Val	Gln	Leu	Met	Leu	His	Phe	Arg	Trp	Asn	Trp	Ile	Ile	Val	195	200	205	
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Glu	Arg	Val	Ala	Arg	Arg	Asp	Ile	Cys	Ile	Ala	Phe	Gln	Glu	Thr	Leu	225	230	235	240
Pro	Thr	Leu	Gln	Pro	Asn	Gln	Asn	Met	Thr	Ser	Glu	Glu	Arg	Gln	Arg	245	250	255	
Leu	Val	Thr	Ile	Val	Asp	Lys	Leu	Gln	Gln	Ser	Thr	Ala	Arg	Val	Val	260	265	270	
Val	Val	Phe	Ser	Pro	Asp	Leu	Thr	Leu	Tyr	His	Phe	Phe	Asn	Glu	Val	275	280	285	
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Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu  
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Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe  
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Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser  
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Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu  
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Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu  
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<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
PDZIP peptide sequence

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<210> 23

<211> 3563

<212> DNA

<213> Homo sapiens

<400> 23

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<210> 24

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Six-His tag

<400> 24

His His His His His His

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5